



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_p2n model

Run on: May 27, 2005, 09:16:26 ; Search time 816.Seconds

(without alignments)  
3408.358 Million cell updates/sec

Title: US-10-054-534B-14

Perfect score: 2415  
Sequence: 1 MVGQKAKKISWATIREHNR.....EVVHLRISIEPFKEPPAM 453

Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Rgapop 6.0 , Rgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=x1h  
-Q=/cgn2\_1/USPRO.spool/h/US10054534/runat\_26052005\_164255\_18483/APP.query.fasta\_1.647  
-DB=Published Applications NA -OPMT=fastcap -SUFFIX=rnpb -MINMATCH=0.1  
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62  
-TRANS=human40.cdd -LIST=45 -DOCALIGN=200 -THR\_SCORE=pcr -THR\_MAX=100  
-THR\_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0  
-MAXLEN=200000000 -USER=US10054534 @CGN 1.1.480 @runat\_26052005\_164255\_18483  
-NCPU=6 -ICPU=3 -NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DISPATCH=100  
-LONGLOG -DEV TIMEOUT=120 -NARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5  
-RGAPOP=6 -RGAEXT=7 -YGAPOP=10 -YGAEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA.\*

1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2:	/cgn2_6/ptodata/2/pubpna/PCIT_NEW_PUB.seq.*
3:	/cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
5:	/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
6:	/cgn2_6/ptodata/2/pubpna/PCITUS_PUBCOMB.seq.*
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8:	/cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
10:	/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11:	/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12:	/cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13:	/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
14:	/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15:	/cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
16:	/cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
17:	/cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18:	/cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
19:	/cgn2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq.*
20:	/cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
21:	/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
22:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2415	100.0	1362	10 US-09-769-863-13	Sequence 13, Appl1
2	2415	100.0	1362	16 US-10-054-534b-13	Sequence 13, Appl1
3	2415	100.0	1362	16 US-10-431-952-13	Sequence 13, Appl1
4	2415	100.0	1362	16 US-10-776-311-35	Sequence 35, Appl1
5	1537	63.6	1380	9 US-09-967-472B-7	Sequence 7, Appl1
6	1129.5	46.8	1434	17 US-10-250-821-3	Sequence 3, Appl1
7	1129.5	46.8	1434	17 US-10-250-553-3	Sequence 3, Appl1
8	943	39.0	1374	16 US-10-278-391-3	Sequence 1, Appl1
9	943	39.0	1374	16 US-10-840-478-1	Sequence 1, Appl1
10	943	39.0	1374	18 US-10-840-478-25	Sequence 25, Appl1
11	943	39.0	1374	18 US-10-840-325-36	Sequence 36, Appl1
12	943	39.0	1617	19 US-10-776-311-33	Sequence 33, Appl1
13	943	39.0	10328	19 US-10-840-325-129	Sequence 129, Appl1
14	922.5	38.2	8894	19 US-10-840-325-124	Sequence 124, Appl1
15	758	31.4	1578	17 US-10-250-821-7	Sequence 7, Appl1
16	758	31.4	1578	17 US-10-250-553-7	Sequence 7, Appl1
17	758	31.4	15430	17 US-10-250-821-25	Sequence 25, Appl1
18	758	31.4	15430	17 US-10-250-553-25	Sequence 25, Appl1
19	758	31.4	17752	17 US-10-250-821-28	Sequence 28, Appl1
20	758	31.4	17752	17 US-10-250-553-28	Sequence 28, Appl1
21	570.5	23.6	1944	18 US-10-437-963-83761	Sequence 83761, A
22	565.5	23.4	2144	17 US-10-425-114-15122	Sequence 15122, A
23	565.5	23.4	2356	17 US-10-424-599-56986	Sequence 56986, A
24	565	23.4	2054	17 US-10-389-566-288	Sequence 288, A
25	561.5	23.3	1344	16 US-10-340-779A-2	Sequence 2, Appl1
26	557.5	23.1	648	17 US-10-250-821-18	Sequence 18, Appl1
27	557.5	23.1	648	17 US-10-250-553-18	Sequence 18, Appl1
28	551	22.8	2226	17 US-10-424-599-124471	Sequence 124471, A
29	547	22.7	1967	17 US-10-425-114-14991	Sequence 14991, A
30	535	22.2	1702	13 US-10-029-756-26	Sequence 26, Appl1
31	535	22.2	1702	13 US-10-702-777-26	Sequence 26, Appl1
32	528.5	21.9	1685	13 US-10-029-756-4	Sequence 4, Appl1
33	528.5	21.9	1685	13 US-10-702-777-4	Sequence 4, Appl1
34	522.5	21.6	1350	9 US-09-938-842A-558	Sequence 558, App
35	522.5	21.6	1350	11 US-09-938-842A-558	Sequence 558, App
36	522.5	21.6	1828	17 US-10-425-114-14869	Sequence 14869, A
37	522.5	21.6	1883	18 US-10-739-930-3353	Sequence 3353, Ap
38	522.5	21.6	1940	17 US-10-424-599-36789	Sequence 36789, A
39	513.5	21.3	1302	18 US-10-437-963-83759	Sequence 83759, A
40	512.5	21.2	1362	19 US-10-504-424-3	Sequence 3, Appl1
41	510.5	21.1	1503	18 US-10-767-795-879	Sequence 879, App
42	500.5	20.7	1362	19 US-10-504-424-1	Sequence 1, Appl1
43	498.5	20.6	1335	17 US-10-239-652A-4	Sequence 4, Appl1
44	498.5	20.6	3016	17 US-10-429-160-25	Sequence 25, Appl1
45	498.5	20.6	3149	17 US-10-172-118-1010	Sequence 1010, Ap

## ALIGNMENTS

RESULT 1  
US-09-769-863-13  
; Sequence 13, Application US/09769863  
; Publication No. US20030157144A1  
; GENERAL INFORMATION:  
; APPLICANT: Abbott Laboratories  
; APPLICANT: Mukerji, Pradip  
; APPLICANT: Huang, Yung-Sheng  
; APPLICANT: Dae, Tapas  
; APPLICANT: Thumond, Jemiffer  
; APPLICANT: Pereira, Suzette L.  
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
; FILE REFERENCE: 6763 US-01  
; CURRENT APPLICATION NUMBER: US/09/769, 863  
; CURRENT FILING DATE: 2001-01-25  
; NUMBER OF SEQ ID NOS: 32  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 1362  
; TYPE: DNA

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## OM protein - nucleic search, using frame\_p1n model

Run on: May 27, 2005, 08:55:06 ; Search time 249 Seconds

(without alignments)  
2976.841 Million cell updates/sec

Title: US-10-054-534B-14

Perfect score: 2415  
Sequence: 1 MVGGQKAKKXISWATIRREHNR.....EVVYHMERISIEPFKEKPPAM 453

## Scoring table:

BLOSUM62	
Xgapop 10.0 , Xgapext 0.5	
Ygapop 10.0 , Ygapext 0.5	
Fgapop 6.0 , Fgapext 7.0	
Delop 6.0 , Delext 7.0	

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Command line parameters:

-MODEL=frame+p1n.model -DEV=x1h  
-Q=/cgn2\_1/USPRO.spool.h/US10054534/runat\_26052005\_164253\_18411/app\_query.fasta\_1.647  
-DB=Issued\_Patents\_NA -OPMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOPT=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdt  
-LIST=45 -DOCLALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000  
-USPR=US10054534\_QCGN\_1\_1\_66@runat\_26052005\_164253\_18411 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6  
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

## Database :

Issued\_Patents\_NA.\*  
1: /cgn2\_6/ptodata/1/ina/5A.COMB.seq.\*  
2: /cgn2\_6/ptodata/1/ina/5B.COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A.COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B.COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS.COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2415	100.0	1362	4	US-09-769-863-13
2	943	39.0	1617	2	US-08-834-655-1
3	943	39.0	1617	3	US-08-834-033A-1
4	943	39.0	1617	3	US-09-363-574-1
5	943	39.0	1617	3	US-09-363-526-1
6	943	39.0	1617	3	US-09-330-235-17
7	644.5	26.7	1281	4	US-09-857-583B-3
8	561.5	23.3	1461	4	US-09-857-583B-1
9	535	22.2	1702	4	US-08-934-254-26
10	528.5	21.9	1684	2	US-09-685-775-1
11	528.5	21.9	1684	2	US-08-831-570-1
12	528.5	21.9	1684	2	US-08-831-575-1

13	528.5	21.9	1685	1	US-08-366-779-4	Sequence 4, Appl1
14	528.5	21.9	1685	1	US-08-789-936-4	Sequence 4, Appl1
15	528.5	21.9	1685	4	US-08-934-254-4	Sequence 4, Appl1
16	528.5	21.9	1685	4	US-09-685-775-4	Sequence 4, Appl1
17	498.5	20.6	3158	4	US-09-949-016-4613	Sequence 4613, Ap
18	489.5	20.3	2257	3	US-09-439-261-8	Sequence 8, Appl1
19	489.5	20.3	2257	3	US-09-227-613-8	Sequence 8, Appl1
20	487.5	20.2	1335	3	US-09-439-261-1	Sequence 1, Appl1
21	487.5	20.2	1335	3	US-09-227-613-1	Sequence 1, Appl1
22	487.5	20.2	1335	3	US-09-439-261-1	Sequence 1, Appl1
23	485.5	20.1	1928	4	US-09-048-888-4	Sequence 4, Appl1
24	449.5	18.6	1758	4	US-09-048-888-2	Sequence 2, Appl1
25	364	15.1	1320	4	US-09-949-016-4904	Sequence 4904, Ap
26	342	14.2	1843	3	US-09-769-863-28	Sequence 28, Appl1
27	342	14.2	1843	3	US-09-439-261-7	Sequence 7, Appl1
28	335	13.9	1413	4	US-09-769-863-19	Sequence 19, Appl1
29	323.5	13.4	864	3	US-09-439-261-12	Sequence 12, Appl1
30	323.5	13.4	864	3	US-09-227-613-13	Sequence 13, Appl1
31	312	12.9	990	3	US-09-439-261-35	Sequence 35, Appl1
32	312	12.9	990	3	US-09-227-613-34	Sequence 34, Appl1
33	304	12.6	918	3	US-09-439-261-5	Sequence 5, Appl1
34	304	12.6	918	3	US-09-227-613-5	Sequence 5, Appl1
35	303	12.5	960	3	US-09-439-261-36	Sequence 36, Appl1
36	303	12.5	960	3	US-09-227-613-35	Sequence 35, Appl1
37	295	12.2	1478	4	US-09-148-545-63	Sequence 63, Appl1
38	286.5	11.9	1482	3	US-09-330-235-11	Sequence 11, Appl1
39	286.5	11.9	1483	2	US-08-833-610-1	Sequence 1, Appl1
40	286.5	11.9	1483	4	US-09-377-452-1	Sequence 1, Appl1
41	284	11.8	1686	3	US-09-439-261-6	Sequence 6, Appl1
42	284	11.8	1686	3	US-09-227-613-6	Sequence 6, Appl1
43	241	10.0	2016	4	US-09-148-545-119	Sequence 119, App
44	237	9.8	1884	1	US-08-307-382-3	Sequence 3, Appl1
45	237	9.8	1884	1	US-08-366-779-3	Sequence 3, Appl1

## ALIGNMENTS

RESULT 1  
US-09-769-863-13  
; Sequence 13, Application US/09769863  
; Patent NO. 6635451  
; GENERAL INFORMATION:

APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pradip  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Das, Tapas  
APPLICANT: Thumond, Jennifer  
APPLICANT: Pereira, Suzette L.  
TITLE OR INVENTION: DESATURASE GENES AND USES THEREOF  
FILE REFERENCE: 6763 US-01  
CURRENT FILING DATE: 2001-01-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 1362  
TYPE: DNA  
ORGANISM: Saprolegnia diclina  
US-09-769-863-13

## Alignment Scores:

Pred. No.: 1.77e-299  
Score: 2415.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 4  
Gaps: 0

US-10-054-534B-14 (1-453) x US-09-769-863-13 (1-1362)  
Cy 1 MetValGlnGlyValGlnValAlaGlyValGlyLeuSerTrpAlaThrIleArgGluHisAsnArg 20  
Db 1 ATGTGTCAGGGGGCAAAAGCCGAGAAAGATCTCTGTGGCCACATCTCTGAGCACACACCGC 60

GenCore version 5.1.6  
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# OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 27, 2005, 08:48:31 ; Search time 759 Seconds  
(without alignments)  
3533.126 Million cell updates/sec

Title: US-10-054-534B-14  
Perfect score: 2415  
Sequence: 1 MVOCQKAEKISWATIREHNR.....EYVHLERISIEFFKEPPAM 453

Scoring table:  
BLOSUM62  
Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 4390206 segs, 2959870667 residues  
Total number of hits satisfying chosen parameters: 8780412

Minimum DB seg length: 0  
Maximum DB seg length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-O=/cgn2.1/USPTO\_epool\_h/US10054534/runat\_26052005\_164252\_18381/app\_query.fasta\_1.647  
-DB=N\_Geneseq -QFMT=fastap -SUFFIX=ing -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human0.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=plco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10054534 @cgn 1\_1\_470@runat\_26052005\_164252\_18381 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEOQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOC  
-DEV TIMEOUT=150 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: N\_Geneseq\_16dec04:\*  
2: Geneseq1980s:\*  
3: Geneseq1990s:\*  
4: Geneseq2000s:\*  
5: Geneseq2001as:\*  
6: Geneseq2002as:\*  
7: Geneseq2002bs:\*  
8: Geneseq2003as:\*  
9: Geneseq2003bs:\*  
10: Geneseq2003cs:\*  
11: Geneseq2003ds:\*  
12: Geneseq2004as:\*  
13: Geneseq2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	2415	100.0	1362 8	AAD49064 Saprolegn
2	2415	100.0	1362 13	ADR20162 Saprolegn
3	1537	63.6	1380 6	AAD35090 Pythium 1
4	1129.5	46.8	1434 6	ABV74258 Phaeodact
5	1129.5	46.8	1434 6	ABQ76780 P. tricolor

6	1129.5	46.8	1443 13	ADR49337 Phaeodact
7	1129.5	46.8	1706 13	ADR49339 Plasmid p
8	943	39.0	1374 5	AAD47129 Fungal de
9	943	39.0	1374 5	AAD25234 Nucleotid
10	943	39.0	1617 2	AAV63624 cDNA enco
11	943	39.0	1617 2	AAV63624 cDNA enco
12	943	39.0	1617 2	AAV63624 cDNA enco
13	943	39.0	1617 2	AAV63624 cDNA enco
14	943	39.0	1617 2	AAV63624 cDNA enco
15	818	33.9	1617 13	ADR20160 Mortiere
16	817	33.8	1604 8	AAV76916 Nucleotid
17	798.5	33.1	2047 4	AAE25730 C. purpur
18	798.5	33.1	2047 4	AAE25730 C. purpur
19	758	31.4	1578 6	ABV74260 Physcomit
20	758	31.4	1578 6	ABV74260 Physcomit
21	758	31.4	1578 6	ABV74260 Physcomit
22	758	31.4	2012 4	AAE26040 P. patens
23	758	31.4	2012 4	AAE26040 P. patens
24	758	31.4	15430 6	ABV74274 Plant spe
25	758	31.4	15430 6	ABV74274 Plant spe
26	758	31.4	17752 6	ABV74275 Plant spe
27	758	31.4	17752 6	ABV74275 Plant spe
28	758	31.4	17752 6	ABV74275 Plant spe
29	631.5	26.1	1266 12	ADP87980 Euglena g
30	613	25.4	1275 3	AAE51233 E. gracil
31	588.5	24.4	1463 3	AAE51233 E. gracil
32	571	23.6	1764 2	AAE51233 E. gracil
33	565	23.3	2054 12	ADU48284 Maize oil
34	561.5	23.3	1344 8	ABX13451 C. elegan
35	561.5	23.3	1344 8	ABX13451 C. elegan
36	561.5	23.3	1344 12	ADP87986 Ceratodon
37	561.5	23.3	1461 3	AAE51232 C. elegan
38	561.5	23.1	1606 3	AAE44851 Sphingoli
39	557.5	23.1	648 6	ABV74268 Phaeodact
40	557.5	23.1	648 6	ABV74268 Phaeodact
41	550	22.8	1972 3	ADU01353 Wheat sph
42	535.5	22.2	1696 12	ADU01558 Evening p
43	535	22.2	1702 8	ABK49503 DNA encod
44	535	22.2	1702 8	ABK49503 DNA encod
45	535	22.2	1702 8	ABK49503 DNA encod

## ALIGNMENTS

RESULT 1	
AAD49064	standard; DNA; 1362 BP.
ID	AAD49064
AC	AAD49064
DT	07-MAR-2003 (first entry)
XX	
DE	Saprolegnia diclina delta 6 desaturase DNA.
XX	
KW	Delta 5 desaturase; delta 6 desaturase; polyunsaturated fatty acid; PUFA;
KW	angioplasty; osteoporosis; inflammation; rheumatoid arthritis; psoriasis;
KW	premature; myalgic encephalitis; chronic fatigue; vasodilation;
KW	acquired immune deficiency syndrome; AIDS; multiple sclerosis; vitreous;
KW	osteopathic; litholytic; nephrotropic; neuroprotective; anticonvulsant;
KW	therapy; antidiabetic; hypotensive; kidney stone; cachexia; cyclostatic;
KW	ecremi; cancer; asthma; enzyme; gene; da.
OS	Saprolegnia diclina.
XX	
FT	Key
FT	CDS
FT	1..1362
FT	Location/Qualifiers
FT	/*tag= a
FT	/product= "Saprolegnia diclina delta 6 desaturase"
XX	
XX	MO200281668-A2.
XX	17-OCT-2002.

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: May 27, 2005, 08:49:06 ; Search time 6201 Seconds

(without alignments)  
3539.786 Million cell updates/sec

Title: US-10-054-534B-14

Perfect score: 2415

Sequence: 1 MVGCGKAKKISMTATREHNR.....EVVHLERISIEFFKPPPM 453

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame\_plus\_p2n.model -DEV=xlh  
-O=/cgn2\_1/USPTO\_spool\_h/US10054534/runac\_26052005\_164252\_18387/app\_query.fasta\_1.647  
-DB=genEmbl -QMT=fastrap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10054534 @CGN 1.1 3731 @runac\_26052005\_164252\_18387 -ICPU=6 -ICPU=3  
-NO\_WMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:\*  
1: gb\_da:\*  
2: gb\_hcg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2415	100.0	1362	6 AR410195
2	2415	100.0	1362	6 AR410195 Sequence
3	1537	63.6	1380	6 AX576988 Sequence
4	1537	63.6	1380	8 AX467717 Sequence
				AP419296 Pythium 1

5	1129.5	46.8	1434	6 AX481613	AX481613 Sequence
6	1129.5	46.8	1434	6 AX481942	AX481942 Sequence
7	1129.5	46.8	1434	6 AX951573	AX951573 Sequence
8	1129.5	46.8	1434	6 CQ874877	CQ874877 Sequence
9	1129.5	46.8	1669	6 AY082393	AY082393 Phaeodact
10	1129.5	46.8	17061	6 CQ874879	CQ874879 Sequence
11	944	39.0	1590	6 AB020032	AB020032 Mortifera
12	943	39.0	1374	6 BD232180	BD232180 Compositi
13	943	39.0	1374	6 AX951591	AX951591 Sequence
14	943	39.0	1617	6 AR080598	AR080598 Sequence
15	943	39.0	1617	6 AR098439	AR098439 Sequence
16	943	39.0	1617	6 AR136018	AR136018 Sequence
17	943	39.0	1617	6 AR215236	AR215236 Sequence
18	943	39.0	1617	6 AR235375	AR235375 Sequence
19	943	39.0	1617	6 BD082621	BD082621 Methods a
20	943	39.0	1617	6 BD092914	BD092914 Methods a
21	943	39.0	1617	6 AF110510	AF110510 Mortifera
22	940	38.9	1374	6 AF465282	AF465282 Mortifera
23	938	38.8	1374	6 AF306634	AF306634 Mortifera
24	932	38.6	1521	6 AB070555	AB070555 Mortifera
25	921	38.1	1374	6 AF465281	AF465281 Mortifera
26	917	38.0	1374	6 AF307940	AF307940 Mortifera
27	900	37.3	1482	6 AY320288	AY320288 Rhizopus
28	883	36.6	1743	6 AB070556	AB070556 Mortifera
29	856.5	35.5	2207	8 AB070557	AB070557 Mortifera
30	852	35.3	2175	8 AJ601391	AJ601391 Mortifera
31	829.5	34.3	1947	8 AF465283	AF465283 Mortifera
32	822.5	34.1	3175	8 AY583463	AY583463 Marchanti
33	818	33.9	1404	6 BD178222	BD178222 Fatty aci
34	818	33.9	1546	6 AB052086	AB052086 Nucor cir
35	817	33.8	1563	6 AX951575	AX951575 Sequence
36	817	33.8	2160	6 AX058840	AX058840 Sequence
37	817	33.8	2160	6 AX951571	AX951571 Sequence
38	817	33.8	2160	6 CP0250735	CP0250735 Ceratodon
39	798.5	33.1	1467	6 AX058832	AX058832 Sequence
40	798.5	33.1	1467	6 AX951569	AX951569 Sequence
41	798.5	33.1	2040	6 AX058830	AX058830 Sequence
42	798.5	33.1	2040	6 AX951567	AX951567 Sequence
43	798.5	32.5	2040	6 CP0250734	CP0250734 Ceratodon
44	785.5	32.5	1071	8 AF621305	AF621305 Mortifera
45	783	32.4	1537	8 AY583316	AY583316 Rhizopus

#### ALIGNMENTS

RESULT 1  
AR410195  
LOCUS AR410195 1362 bp DNA linear PAT 18-DEC-2003  
DEFINITION Sequence 13 from patent US 6635451.  
ACCESSION AR410195  
VERSION AR410195.1 GI:40161436  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1362)  
AUTHORS Mukerji, P., Huang, Y.-S., Das, T., Thurmond, J. and Pereira, S. L.  
TITLE Desaturase genes and uses thereof  
JOURNAL Patent: US 6635451-A 13 21-OCT-2003;  
FEATURES  
SOURCE 1. 1362  
Location/Qualifiers  
/organism="unknown"  
/mol\_type="genomic DNA"

#### ORIGIN

Alignment Scores:  
Pred. No.: 6.6e-232  
Score: 2415.00  
Percent Similarity: 100.00%  
Best Local Similarity: 100.00%  
Query Match: 100.00%  
DB: 6  
Length: 1362  
Matches: 453  
Conservative: 0  
Mismatch: 0  
Indels: 0  
Gaps: 0

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2005, 05:35:03 ; Search time 388 Seconds  
(without alignments)  
597.866 Million cell updates/sec

Title: US-10-054-534B-14  
Perfect score: 2415  
Sequence: 1 MVQSGQKAKISWATIREHNR.....EYVHLERISIEFFKPPAM 453

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : UniProt\_03:\*  
1: uniprot\_sprotl:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1537	63.6	459	2	0944W4 pythium irr
2	1129.5	46.8	477	2	08RXB0
3	944	39.1	457	2	09UVY3
4	943	39.0	457	2	09UVV3
5	940	38.9	457	2	09UVV3
6	938	38.8	457	2	09HEV4
7	937	38.8	457	2	07OBL2
8	932	38.6	458	2	07ELW8
9	921	38.1	457	2	08X174
10	917	38.0	457	2	09HEV1
11	900	37.3	458	2	06SF62
12	900	37.3	458	2	07ZBP2
13	822.5	34.1	481	2	0696V8
14	818	33.9	467	2	096VC3
15	818	33.9	467	2	06TMX2
16	817	33.8	520	2	09LEW9
17	798.5	33.1	483	2	09LEW9
18	785.5	32.5	357	2	06IV28
19	779.5	32.3	357	2	09HDF4
20	758	31.4	525	2	092NM2
21	758	31.4	525	2	092NM2
22	613	25.4	419	2	09SKW9
23	586.5	24.3	443	2	023221
24	585.5	24.2	443	2	061388
25	570.5	23.6	466	2	06ERL2
26	561.5	23.3	447	2	09XTB7
27	558.5	23.1	458	2	043469
28	558	23.1	446	2	08LBD7
29	549	22.7	469	2	092TUB
30	533.5	22.1	464	2	0696V5
31	532	22.0	446	2	071BG4

ALIGNMENTS									
RESULT 1									
ID	Q944W4	PRELIMINARY;	PRT;	459 AA.					
AC	Q944W4;								
DT	01-DEC-2001 (TREMBLrel. 19, Created)								
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)								
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)								
DS	Delta-6 fatty acid desaturase.								
OS	Pythium irregulare.								
OC	Eukaryota; stramenopiles; Oomycetes; Pythiales; Pythiaceae; Pythium.								
OX	NCBI_Taxid=36331;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RA	Hong H., Datta N., Mackenzie S.L., Qiu X.;								
RL	Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.								
CC	-1- SIMILARITY: Belongs to the fatty acid desaturase family.								
DR	EMBL; AF419296; AAL3310.1; -								
DR	HSSP; P04166; 1BSM.								
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.								
DR	GO; GO:0006633; P:fatty acid biosynthesis; IEA.								
DR	InterPro; IPR008938; ARM.								
DR	InterPro; IPR001199; Cyt B5.								
DR	InterPro; IPR005804; Fa_desat.								
DR	InterPro; IPR010257; Fa_desat_sub.								
DR	Pfam; PF00173; Cyt-B5; 1.								
DR	Pfam; PF00487; FA_desaturase; 1.								
DR	ProDom; PD000612; Cyt B5; 1.								
DR	ProDom; PD001081; FA_desat_sub; 1.								
DR	PROSITE; PS02055; CYTOCHROME_B5_2; 1.								
KW	Fatty acid biosynthesis; Heme; Lipid synthesis; Oxidoreductase.								
SQ	SEQUENCE 459 AA; 52498 MW; 286464IDA/61BR055 CRC64;								
Query Match 63.6%; Score 1537; DB 2; Length 459;									
Best Local Similarity 62.8%; Pred. No. 5e-124;									
Matches 282; Conservative 68; Mismatches 93; Indels 6; Gaps 3									
QY	10 ISWATIREHNRQDNAMVITHHKVYDISAFEDPGGVWFTQAGBDATDAFAVTHSSALK 69								
Db	12 VSMKEIREHATPATAMVITHHKVYDISKMDHPGGSVWLTAQGEDATDAFAVTHSSALK 71								
QY	70 LLEQYVGGDVDSIA--VDTSIDVYKKSQ--SDFLASRKLRLRYRGLYDSSTLY 124								
Db	72 LLEQFYGGDVDETSEKATIEGPADDERARERINEFLASRYRLRVKVGKGLDYASALY 131								
QY	125 YLYKCASTLSIALYSAALCLHFDSTAMVMAVAALVILGYOOCGMALHFLHNOVENLIF 184								
Db	132 YAMLVSTFGIALVSMALCFPFNSPATMVAAGVIMGLFTQOSGMALHFLHNOVCENRTL 191								
QY	185 GDLVGVVGNLMQSFVQVMKRNKNTHTALPNLHATPEIAFHCDPDIDTWELMWSLMA 244								
Db	192 GNILGCLVGNAMQSFVQVMKRNKNTLHNAVPLNLSADDEGFIQDPDIDTWELMWSKMA 251								
QY	245 QHAYDSVGLFPRRYQALVLPPIILFARISVAVIOSAMTAPFNNGVGGTFDYQVQPILERA 304								

## ALIGNMENTS

Query Match	Score	Length	ID	Description
10	ISMTTIRHNRQDNAAVTHHKKYDIAFEBHPCGVMTFQAGSDATDAFVPPSSALX	69		
12	VSMKEIRERHATPATVATVTHHKKYDIAFEBHPCGVMTFQAGSDATDAFVPPSSALX	71		
70	LLBOYVYDVNDQFAA--VPTSIDBVKKSQ---SDFIASRYKRLVFRGRLGLDVSSTLY	124		
125	YLKVCATLSTALVSAALICLHFDSTAMVVAATLGLFYQCGWLAHDFLHFOVENLIF	184		
132	YAMLVSTFGIALVSMALICFPFNSFAMVVAATLGLFYQCGWLAHDFLHFOVENLIF	191		
185	GDIVGVAVGNTLQFSGVQWKKKNTTHAIPNLHATBEIAFHGPPDIDTPELILWSLMA	244		
192	GNLIGCLVGNAMQFVSQWKKKNTTHAIPNLHATBEIAFHGPPDIDTPELILWSLMA	251		
245	QHAVDSPVGLFPRYQVLYFPIILFARISVLIQSNAMVAFYVNGPGGTPDVQVPLLEBA	304		

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: May 27, 2005, 07:12:09 ; Search time 74 Seconds  
(without alignments)  
589.003 Million cell updates/sec

Title: US-10-054-534B-14

Perfect score: 2415  
Sequence: 1 MVQGGKAKKISMATIREHNR.....EYVHLERISIEFPKPPAM 453

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_79:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	567.5	23.5	473	1 T6280	linoleoyl-CoA dea
2	567.5	23.3	447	1 T4319	Delta6 fatty acid
3	558.5	23.1	458	2 S68358	Delta8 sphingolip
4	548	22.7	454	2 H88791	protein T13P2.1 [i
5	522.5	21.6	449	2 T47950	delta-8 sphingolip
6	521.5	21.6	449	2 T50555	hypothetical prote
7	519.5	21.5	449	2 A84900	linoleoyl-CoA dea
8	498.5	20.6	444	2 T13155	Delta6 fatty acid
9	487.5	20.2	523	2 JG0180	linoleoyl-CoA dea
10	456.5	18.9	523	2 JG7556	linoleoyl-CoA dea
11	399	16.5	345	2 T36617	probable Delta6 fa
12	237	9.8	359	2 S35157	Delta6 fatty acid
13	208	8.6	368	2 S34809	linoleoyl-CoA dea
14	195	8.1	134	2 T00796	cytochrome b5 Ac2g
15	189	7.8	139	2 S46306	cytochrome b5 - co
16	187	7.7	140	2 T52468	cytochrome b5 [imp
17	184.5	7.6	135	2 A86390	hypothetical prote
18	183	7.6	909	2 JN0665	nitrate reductase
19	182	7.5	120	2 S63052	cytochrome b5 - ye
20	181	7.5	911	2 RDT0NH	nitrate reductase
21	180.5	7.5	135	2 S49200	cytochrome b5 - co
22	180	7.5	137	2 S46307	cytochrome b5 - r1
23	178	7.4	135	2 JG7671	ascidian cytochrom
24	171	7.1	889	2 T02240	nitrate reductase
25	167.5	6.9	135	2 T09946	cytochrome b5 - so
26	167	6.9	884	2 S66308	nitrate reductase
27	166.5	6.9	132	2 E84905	probable cytochrom
28	166.5	6.9	920	2 S52301	nitrate reductase
29	166	6.9	134	2 T14454	cytochrome b5 - w1

30	166	6.9	900	2 S47029	nitrate reductase
31	165.5	6.9	911	2 T08105	nitrate reductase
32	165	6.8	886	2 A59223	nitrate reductase
33	164.5	6.8	891	1 RDBHNP	nitrate reductase
34	164.5	6.8	917	2 B96807	nitrate reductase
35	164.5	6.8	917	2 S35228	nitrate reductase
36	164	6.8	881	2 S25445	nitrate reductase
37	162	6.7	134	2 T52469	cytochrome b5 [imp
38	162	6.7	427	2 G70590	probable desA3 pro
39	162	6.7	916	2 S07554	nitrate reductase
40	161.5	6.7	904	1 RDNNTM	nitrate reductase
41	161.5	6.7	911	2 T08108	nitrate reductase
42	160.5	6.6	904	1 RDNNTS	nitrate reductase
43	159	6.6	890	2 T11805	nitrate reductase
44	158.5	6.6	898	1 RDBJNH	nitrate reductase
45	157.5	6.5	424	2 JG5891	omega 6 desaturase

## ALIGNMENTS

## RESULT 1

T6280 linoleoyl-CoA desaturase (EC 1.14.19.3) W0802.4 - Caenorhabditis elegans

N/Alternate names: Delta6 fatty acid desaturase

C/Species: Caenorhabditis elegans

C/Date: 09-Jun-2000 #sequence\_revision 09-Jun-2000 #text\_change 09-Jul-2004

C/Accession: T6280, T37238

R/Swblurne, J.; Ainecough, R.

submitted to the EMBL Data Library, March 1996

A/Reference number: Z20188

A/Accession: T6280

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-473 <Wtl>

A/Cross-references: UNIPROT:O61388, EMBL:Z70271, PIDN:CA94233.1, GSPDB:GN00022, CESP:W

A/Cross-references: EMBL:AF031477, NID:G308619, PIDN:AAC1586.1, PID:G3086520

C/Genetics:

A/Gene: CESP:W0802.4

A/Map position: 4

A/Introns: 13/3; 234/3; 277/3; 378/1; 413/3

A/Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by het

A/Reference number: Z21637, MUID:9814972, PMID:9480865

A/Accession: T37238

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-38,59-430,'V',432-473 <NAP>

A/Cross-references: EMBL:AF031477, NID:G308619, PIDN:AAC1586.1, PID:G3086520

C/Genetics:

A/Gene: CESP:W0802.4

A/Map position: 4

A/Introns: 13/3; 234/3; 277/3; 378/1; 413/3

A/Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by het

A/Reference number: Z21637, MUID:9814972, PMID:9480865

A/Accession: T37238

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-38,59-430,'V',432-473 <NAP>

A/Cross-references: EMBL:AF031477, NID:G308619, PIDN:AAC1586.1, PID:G3086520

C/Genetics:

A/Gene: CESP:W0802.4

A/Map position: 4

A/Introns: 13/3; 234/3; 277/3; 378/1; 413/3

A/Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by het

A/Reference number: Z21637, MUID:9814972, PMID:9480865

A/Accession: T37238

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-38,59-430,'V',432-473 <NAP>

A/Cross-references: EMBL:AF031477, NID:G308619, PIDN:AAC1586.1, PID:G3086520

C/Genetics:

A/Gene: CESP:W0802.4

A/Map position: 4

A/Introns: 13/3; 234/3; 277/3; 378/1; 413/3

A/Title: Identification of a caenorhabditis elegans Delta6-fatty-acid-desaturase by het

A/Reference number: Z21637, MUID:9814972, PMID:9480865

A/Accession: T37238

A/Status: preliminary; translated from GB/EMBL/DBJ



Result No.	Score	Query Match	Length	DB	ID	Description
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2	2415	100.0	453	14	US-10-054-534B-14	Sequence 14, Appl
3	2415	100.0	453	14	US-10-431-952-14	Sequence 14, Appl
4	2415	100.0	453	16	US-10-776-311-36	Sequence 16, Appl
5	1537	63.6	459	9	US-09-967-477B-8	Sequence 8, Appl
6	1129.5	46.8	477	15	US-10-250-821-4	Sequence 4, Appl
7	1129.5	46.8	477	15	US-10-250-553-4	Sequence 4, Appl
8	943	39.0	457	14	US-10-278-331-4	Sequence 4, Appl
9	943	39.0	457	16	US-10-776-311-36	Sequence 16, Appl
10	943	39.0	457	17	US-10-840-335-37	Sequence 37, Appl
11	943	39.0	458	14	US-10-191-513A-11	Sequence 11, Appl
12	943	39.0	458	14	US-10-191-513A-41	Sequence 41, Appl
13	758	31.4	525	15	US-10-250-821-8	Sequence 8, Appl

45	494	20.5	432	14	US-10-191-513A-9	Sequence 9, April
44	498.5	20.6	473	15	US-10-239-655A-8	Sequence 8, April
43	498.5	20.6	444	15	US-10-239-655A-7	Sequence 7, April
42	498.5	20.6	444	15	US-10-429-160-26	Sequence 26, April
41	500.5	20.7	453	17	US-10-504-424-2	Sequence 2, April
40	512.5	21.2	453	17	US-10-504-424-4	Sequence 4, April
39	518.5	21.5	433	16	US-10-437-963-186242	Sequence 186242, April
38	522.5	21.6	497	15	US-10-425-114-52563	Sequence 52563, April
37	522.5	21.6	451	15	US-10-424-559-179631	Sequence 179631, April
36	522.5	21.6	448	15	US-10-429-779-5	Sequence 5, April
35	522.5	21.6	448	14	US-10-029-756-5	Sequence 5, April
34	527.5	21.8	448	14	US-10-040-779A-13	Sequence 13, April
33	535	22.2	452	15	US-10-702-777-27	Sequence 27, April
32	535	22.2	452	13	US-10-029-756-27	Sequence 27, April
31	548	22.7	454	15	US-10-369-493-6107	Sequence 6107, April
30	549	22.7	448	14	US-10-340-779A-4	Sequence 4, April
29	551	22.8	448	15	US-10-424-559-267313	Sequence 267313, April
28	557.5	23.1	216	15	US-10-350-553-19	Sequence 19, April
27	557.5	23.1	216	15	US-10-250-821-11	Sequence 11, April
26	558.5	23.1	458	14	US-10-340-779A-11	Sequence 11, April
25	565	23.4	515	15	US-10-389-566-447	Sequence 447, April
24	565.5	23.4	453	15	US-10-425-114-48669	Sequence 48669, April
23	567.5	23.4	448	15	US-10-424-559-199828	Sequence 199828, April
22	567.5	23.6	473	15	US-10-369-493-6108	Sequence 6108, April
21	570.5	23.6	466	16	US-10-437-963-186244	Sequence 186244, April
20	593.5	24.6	443	14	US-10-340-779A-20	Sequence 20, April
19	593.5	24.6	443	14	US-10-191-513A-17	Sequence 17, April
18	758	31.4	525	15	US-10-350-553-30	Sequence 30, April
17	758	31.4	525	15	US-10-350-553-27	Sequence 27, April
16	758	31.4	525	15	US-10-250-821-30	Sequence 30, April
15	758	31.4	525	15	US-10-250-821-27	Sequence 27, April
14	758	31.4	525	15	US-10-250-821-27	Sequence 27, April

## ALIGNMENTS

```

1
US-09-769-863-14
: Sequence 14, Application US/09769863
: Publication NO. US20030157144A1
: GENERAL INFORMATION:
: APPLICANT: Abbott Laboratories
: APPLICANT: Mukerji, Pradip
: APPLICANT: Huang, Yung-Sheng
: APPLICANT: Dae, Tapas
: APPLICANT: Thirumond, Jennifer
: APPLICANT: Pereira, Suzette L.
: TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
: FILE REFERENCE: 6763 US 01
: CURRENT APPLICATION NUMBER: US/09/769,863
: CURRENT FILING DATE: 2001-01-25
: NUMBER OF SEQ ID NOS: 32
: SOFTWARE: FastSeq for Windows Version 4.0.
: SEQ ID NO 14
: LENGTH: 453
: TYPE: prt
: ORGANISM: Saprolegnia diclina
US-09-769-863-14

```

Query	Match	Similarity	100.0%	Score	2415	DB	10	Length	453	
Best	Local	Similarity	100.0%	Pred.	No.	1.9e-230				
Matches	453	Conservative	0	Mismatches	0	Indels	0	Gaps	0	
Qy	1	MVGGQKAEKTSWATREHNRQDNAMIVLHHKYVDISAEVDHPGGVMPFTQAGEBDATDPA	60							
Db	1	MVGGQKAEKTSWATREHNRQDNAMIVLHHKYVDISAEVDHPGGVMPFTQAGEBDATDPA	60							
Qy	61	VFRHSSAKLLEQYVVDVQSTAAVDTSISDEYKKSQSDPTASRYKRLREVKRLGLYDS	120							
Db	61	VFRHSSAKLLEQYVVDVQSTAAVDTSISDEYKKSQSDPTASRYKRLREVKRLGLYDS	120							
Qy	121	SKLYLYLKCASTSIALVSAATCIHPDSTAMTVAAVILGLFYQCCGLAHDFLHHQVE	180							



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# OM protein - protein search, using sw model

Run on: May 27, 2005, 07:55:05 / Search time 28 Seconds  
(without alignments)  
1207.715 Million cell updates/sec

Title: US-10-054-534B-14  
Perfect score: 2415  
Sequence: 1 MVQOKAKESWATIREHNR.....EYVHLERISIEFKPEPPAM 453

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCUTS\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2415	100.0	453	4	US-09-769-863-14
2	943	39.0	457	2	US-08-834-655-2
3	943	39.0	457	2	US-08-833-610-4
4	943	39.0	457	3	US-08-834-033A-2
5	943	39.0	457	3	US-08-834-033A-14
6	943	39.0	457	3	US-09-363-574-2
7	943	39.0	457	4	US-09-363-526-2
8	943	39.0	457	4	US-09-330-235-18
9	943	39.0	457	4	US-09-377-452-4
10	943	39.0	458	4	US-09-439-261-10
11	943	39.0	458	4	US-09-439-261-44
12	943	39.0	458	4	US-09-227-613-11
13	943	39.0	458	4	US-09-227-613-41
14	775.5	32.1	355	2	US-08-834-655-5
15	775.5	32.1	355	2	US-08-834-033A-6
16	775.5	32.1	355	3	US-09-363-574-5
17	775.5	32.1	355	4	US-09-363-526-5
18	713.5	29.5	323	4	US-09-439-261-17
19	713.5	29.5	323	4	US-09-227-613-17
20	644.5	26.7	421	4	US-09-857-583B-4
21	586.5	24.3	443	4	US-09-857-583B-14
22	561.5	23.3	447	4	US-09-857-583B-2
23	535	22.2	452	3	US-08-934-254-27
24	535	22.2	452	4	US-09-685-775-27
25	527.5	21.8	448	4	US-09-857-583B-15
26	526.5	21.8	446	2	US-08-833-610-5
27	526.5	21.8	446	3	US-08-834-033A-15

28	526.5	21.8	446	4	US-09-377-452-5	Sequence 5, Appli
29	522.5	21.6	448	1	US-08-366-779-5	Sequence 5, Appli
30	522.5	21.6	448	1	US-08-789-936-5	Sequence 5, Appli
31	522.5	21.6	448	3	US-08-934-254-5	Sequence 5, Appli
32	522.5	21.6	448	4	US-09-685-775-5	Sequence 5, Appli
33	498.5	20.6	498	4	US-09-949-016-10484	Sequence 10484, A
34	494	20.5	432	4	US-09-439-261-9	Sequence 9, Appli
35	494	20.5	432	4	US-09-227-613-9	Sequence 9, Appli
36	494	20.5	465	4	US-09-439-261-40	Sequence 40, Appli
37	494	20.5	465	4	US-09-227-613-38	Sequence 38, Appli
38	487.5	20.2	444	4	US-09-439-261-11	Sequence 11, Appli
39	487.5	20.2	444	4	US-09-227-613-12	Sequence 12, Appli
40	487.5	20.2	445	4	US-09-439-261-39	Sequence 39, Appli
41	487.5	20.2	445	4	US-09-439-261-45	Sequence 45, Appli
42	485.5	20.1	444	4	US-09-048-888-3	Sequence 3, Appli
43	478	19.8	444	4	US-09-439-261-43	Sequence 43, Appli
44	478	19.8	444	4	US-09-227-613-42	Sequence 42, Appli
45	449.5	18.6	445	4	US-09-048-888-1	Sequence 1, Appli

## ALIGNMENTS

RESULT 1  
US-09-769-863-14  
Sequence 14, Application US/09769863  
Patent No. 6635451  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pradip  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Dae, Tapae  
APPLICANT: Thurmond, Jennifer  
APPLICANT: Pereira, Suzette L.  
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
FILE REFERENCE: 6763. US. 01  
CURRENT FILING DATE: 2001-01-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 14  
LENGTH: 453  
TYPE: PRT  
ORGANISM: Saprolegnia diclina  
US-09-769-863-14

Query Match	100.0%; Score 2415; DB 4; Length 453;
Best Local Similarity	100.0%; Pred. No. 2.4e-259;
Matches 453; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MVQOKAKESWATIREHNRQDNAMVIYHKKYDISAFEDHGVVMEVTOGEBATDAFA 60
DB	1 MVQOKAKESWATIREHNRQDNAMVIYHKKYDISAFEDHGVVMEVTOGEBATDAFA 60
QY	61 VFHSSALKLLEQYVVDVOSTAANDTSISDEYKKSQSDPIASYRKLREYKGLGYS 120
DB	61 VFHSSALKLLEQYVVDVOSTAANDTSISDEYKKSQSDPIASYRKLREYKGLGYS 120
QY	121 SKLYTYKCASTSTIALVSAICLHFDSTAMVVAAYILGLFYQCCGLANDPLHQVFE 180
DB	121 SKLYTYKCASTSTIALVSAICLHFDSTAMVVAAYILGLFYQCCGLANDPLHQVFE 180
QY	181 NMLFGDLGVWVGNLWQGFVSQVWKNKXNTHAIPNLHATPEIAFHGDPDIDTPIILAMS 240
DB	181 NMLFGDLGVWVGNLWQGFVSQVWKNKXNTHAIPNLHATPEIAFHGDPDIDTPIILAMS 240
QY	241 LKKAQHADVSPVGLFFEMRYQAYLYEPILLFARISWVOSAMVAYRNGRGTPEKVOYPL 300
DB	241 LKKAQHADVSPVGLFFEMRYQAYLYEPILLFARISWVOSAMVAYRNGRGTPEKVOYPL 300
QY	301 LERAGLLLYTGWNLGYLYAANMSILQAAFLFVSQASCGLFLANVFSVGNHGMVFPDQDS 360
DB	301 LERAGLLLYTGWNLGYLYAANMSILQAAFLFVSQASCGLFLANVFSVGNHGMVFPDQDS 360

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OM protein - protein search, using sw model

Run on: May 27, 2005, 05:30:42 ; Search time 318 Seconds

(without alignments)  
550.951 Million cell updates/sec

Title: US-10-054-534B-14

Perfect score: 2415  
Sequence: 1 MVQOQKAEKISWATIREHR.....EYVHLERISIEPFKEPPAM 453

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database: A\_Geneseq\_16Dec04:\*

1: geneseqp1980s:\*\n2: geneseqp1990s:\*\n3: geneseqp2000s:\*\n4: geneseqp2001s:\*\n5: geneseqp2002s:\*\n6: geneseqp2003as:\*\n7: geneseqp2003bs:\*\n8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	2415	100.0	AAE31900	Saprolegn
2	2415	100.0	ADR20163	ADR20163
3	1537	63.6	AAE22063	Pythium I
4	1129.5	46.8	ABE98275	Phaeodact
5	1129.5	46.8	ABG73600	P. tricolor
6	1129.5	46.8	ADR49338	Phaeodact
7	1129.5	46.8	ADR49342	Phaeodact
8	943	39.0	AAW84137	A delta-6
9	943	39.0	AAW95504	Mortierel
10	943	39.0	AAW85121	A delta-6
11	943	39.0	AAW56045	Fungal de
12	943	39.0	AAV92599	M. alpina
13	943	39.0	AAW31684	Amino aci
14	943	39.0	ADR20161	Mortierel
15	943	39.0	ABG96527	M. alpina
16	943	39.0	ABG96509	M. alpina
17	943	39.0	ABG94707	Human del
18	943	39.0	ABG94693	Human del
19	818	33.9	ABW99479	Amino aci
20	817	33.8	ABW46440	C. purpur
21	798.5	33.1	ABW46436	C. purpur
22	798.5	33.1	ABW46435	C. purpur
23	775.5	32.1	AAW84139	Desaturas
24	758	31.4	AAV51354	Protein b
25	758	31.4	AAW46810	P. patens

26	758	31.4	525	5	ABB98277	Phycomit
27	758	31.4	525	5	ABG73602	P. patens
28	758	31.4	525	5	ABG73607	P. patens
29	758	31.4	525	5	ABG73609	P. patens
30	758	31.4	525	8	ADR49326	Phycomit
31	758	31.4	525	8	ADR49315	Phycomit
32	713.5	29.5	323	5	ABG96515	M. alpina
33	713.5	29.5	323	5	ABG96515	M. alpina
34	631.5	26.1	421	8	ADP87981	Human del
35	619.5	25.7	422	8	AAV96722	E. gleria
36	585.5	24.2	443	2	AAV17751	Caenorhab
37	571	23.6	462	3	AAV71552	Corn spm
38	567.5	23.5	473	3	AAV51353	Protein b
39	567.5	23.4	473	8	ADN23455	Bacterial
40	565	23.4	515	8	ADJ48443	Maize oil
41	561.5	23.3	447	2	AAV21891	C. elegan
42	561.5	23.3	447	8	ADP87987	C. elegan
43	561.5	23.3	447	8	ADP87987	C. elegan
44	558.5	23.1	458	3	AAV51348	Sphingoli
45	558.5	23.1	458	7	ADF69394	Cytochrom

## ALIGNMENTS

RESULT 1	AAE31900	standard; protein; 453 AA.
ID	AAE31900	
XX	AAE31900;	
AC		
DT	07-MAR-2003	(first entry)
XX		
DE	Saprolegnia dictina delta 6 desaturase.	
XX		
KW	Delta 5 desaturase; delta 6 desaturase; polyunsaturated fatty acid; PUPA;	Abb98277 Phycomit
KW	angiolaesly; osteoporosis; inflammation; rheumatoid arthritis; psoriasis;	Abg73602 P. patens
KW	premenstrual syndrome; myalgic encephalitis; chronic fatigue; vasotropic;	Abg73607 P. patens
KW	acquired immune deficiency syndrome; AIDS; multiple sclerosis; vitruide;	Abg73609 P. patens
KW	osteopachic; litholytic; nephrotropic; neuroprotective; kidney stone; cachexia; cyrostatic;	Adt49326 Phycomit
KW	therapy; antilipemetic; hypotensive; kidney stone; cachexia; cyrostatic;	Adt49315 Phycomit
KW	eczema; cancer; asthma; enzyme.	ADR49315
XX		
OS	Saprolegnia dictina.	
XX		
FN	WO200281668-A2.	
XX		
PD	17-OCT-2002.	
XX		
XX	24-JAN-2002; 2002MO-US001924.	
PF		
XX	25-JAN-2001; 2001US-00769863.	
PR		
XX	22-JAN-2002; 2002US-00054534.	
XX		
PA	(ABBO) ABBOTT LAB.	
XX		
PI	Mukerji P, Huang Y, Das T, Thurmond J, Pereira SL;	
XX		
DR	WPI; 2003-067519/06.	
XX	N-PSDB; AAD49064.	
PT		
XX	New delta 5 desaturase or delta 6 desaturase polypeptides, useful for	
XX	producing polyunsaturated fatty acids, desaturates polyunsaturated fatty	
XX	acids at carbon 5 and carbon 6, respectively.	
PS	Example 2; Page 148-149; 165pp; English.	
CC	The invention relates to delta 5 desaturase or delta 6 desaturase	
CC	polypeptides and their nucleic acids. These sequences are useful for	
CC	producing polyunsaturated fatty acids (PUPA) by desaturating PUPA at	
CC	carbon 5 and carbon 6. Composition comprising at least one PUPA is useful	
CC	for preventing or treating a condition caused by insufficient intake of	
CC	PUPA. It is useful for treating restenosis after angioplasty, symptoms of	

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OM nucleic - nucleic search, using SW model

Run on: May 27, 2005, 00:44:37 / Search time 8715 Seconds  
(without alignments)  
5948.771 Million cell updates/sec

Title: US-10-054-534B-13

Perfect score: 1362  
Sequence: 1 atggtccaggagcaaaagc.....aggagttcccgcatgtaa 1362

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
EST:  
1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_gss1.\*  
9: gb\_gss2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	96	7.0	819	5	BU745135 CH1#007_D
C 2	93.6	6.9	458	7	CN006019 1p37109.G
C 3	93.6	6.9	600	7	CK9398942 1p37109.B
C 4	93	6.8	390	2	AM052655 r338a08.Y
C 5	92.8	6.8	509	2	BG608740 307418.MA
C 6	92.6	6.8	884	5	B0881930 AGENCOURT
C 7	92	6.8	614	5	BP161817
C 8	91.4	6.7	421	7	CF140245
C 9	91.4	6.7	530	2	AM246354 2822200.5
C 10	91.4	6.7	535	2	BF207014 601870487
C 11	91.4	6.7	581	5	BP252288 BP252288
C 12	91.4	6.7	581	5	BP252288 BP252288
C 13	91.4	6.7	585	5	BP254298 BP254298
C 14	91.4	6.7	585	5	BP254298 BP254298
C 15	91.4	6.7	598	7	CN283566
C 16	91.4	6.7	629	2	BG390559 602416330
C 17	91.4	6.7	633	2	BE331371 601149928
C 18	91.4	6.7	641	2	BE382648 601297091
C 19	91.4	6.7	666	6	CD618242 566611144
C 20	91.4	6.7	689	4	BG696921 602658688
C 21	91.4	6.7	693	5	BU623713 UI-H-FG1-
C 22	91.4	6.7	730	5	BU626230 UI-H-FG1-
C 23	91.4	6.7	753	4	BG422898 602450074
C 24	91.4	6.7	754	4	BG696675 602658982

25	91.4	6.7	783	4	BG743255	BG743255 602633329
26	91.4	6.7	799	5	BG743597	BG743597 602633951
27	91.4	6.7	819	5	BK440551	BK440551 BX440551
28	91.4	6.7	830	4	BG674961	BG674961 602621157
29	91.4	6.7	830	4	BG742494	BG742494 602632324
30	91.4	6.7	840	5	BU195643	BU195643 AGENCOURT
31	91.4	6.7	841	5	BQ423614	BQ423614 AGENCOURT
32	91.4	6.7	882	5	BQ229517	BQ229517 AGENCOURT
33	91.4	6.7	892	6	CA488914	CA488914 AGENCOURT
34	91.4	6.7	894	4	BG743088	BG743088 602634223
35	91.4	6.7	895	4	CA487874	CA487874 AGENCOURT
36	91.4	6.7	903	5	BQ721408	BQ721408 AGENCOURT
37	91.4	6.7	905	4	BG674790	BG674790 602620919
38	91.4	6.7	905	5	BUS27215	BUS27215 AGENCOURT
39	91.4	6.7	922	5	BU156232	BU156232 AGENCOURT
40	91.4	6.7	928	4	BG420045	BG420045 602453732
41	91.4	6.7	935	4	BI199054	BI199054 602759167
42	91.4	6.7	1167	4	BM478339	BM478339 AGENCOURT
43	91.4	6.7	1335	9	AY418548	AY418548 Homo sapi
44	91.2	6.7	489	2	AW231075	AW231075 uc070e04.Y
45	91.2	6.7	834	5	BK455254	BK455254 BX455254

## ALIGNMENTS

RESULT 1  
BU745135/c 819 bp mRNA linear EST 10-OCT-2002  
LOCUS CH1#007\_D09T3 Canine heart non-normalized cDNA Library in  
DEFINITION Bluescript Canis familiaris cDNA clone CH1#007\_D09 3', mRNA  
sequence.  
ACCESSION BU745135 GI:23694297  
VERSION BU745135.1  
KEYWORDS EST.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
REFERENCE 1 (bases 1 to 819)  
Yi, Y., Desai, R., Olarte, M., Henthorn, P. and George A.L.  
Expressed sequence tags from Canine heart  
JOURNAL Unpublished (2003)  
COMMENT Other ESTs: CH1#007\_D09T7  
Contact: George AL  
Division of Genetic Medicine  
Vanderbilt University  
529 Light Hall, 2215 Garland Avenue, Nashville, TN 37232-0275, USA  
Tel: 615 936 2660  
Fax: 615 936 2661  
Email: al.george@vanderbilt.edu  
Insert length: 1655 Std Error: 0.00  
Seq primer: T3: ATTAACTCTCACTAAGGGA  
High quality sequence start: 65  
High quality sequence stop: 628.  
FEATURES  
Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:9615"  
/clone="CH1#007\_D09"  
/tissue\_type="heart"  
/cell\_type="heart"  
/dev\_stage="mixed developmental stages (adult, 30 day - 40 day fetal)"  
/clone\_jib="Canine heart non-normalized cDNA Library in  
bluescript"  
/note="Organ: heart; Vector: bluescript; Site 1: 5' of  
vector NotI; Site 2: 3' of vector EcoRI; Tissue source:  
dog heart (adult, 30 day - 40 day fetal), right and left  
atria and ventricle. Dog breed - mixed (beagle, German  
shepherd, pointer, Irish setter). Library construction:  
oligo-dt primed"

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OM nucleic - nucleic search, using sw model

Run on: May 27, 2005, 03:05:18 ; Search time 2408 Seconds  
(without alignments)  
3472.625 Million cell updates/sec

Title: US-10-054-534B-13

Perfect score: 1362  
Sequence: 1 atggctcaggaggcaaaagc.....aggagttccgcgcattgtaa 1362

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 5700845 seqs, 3069779757 residues

Total number of hits satisfying chosen parameters: 11401690

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/2/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/2/pubpna/US06\_PUBCOMB.seq:\*
- 5: /cgn2\_6/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*
- 6: /cgn2\_6/ptodata/2/pubpna/PCTUS\_PUBCOMB.seq:\*
- 7: /cgn2\_6/ptodata/2/pubpna/US08\_NEW\_PUB.seq:\*
- 8: /cgn2\_6/ptodata/2/pubpna/US08\_PUBCOMB.seq:\*
- 9: /cgn2\_6/ptodata/2/pubpna/US09A\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1362	100.0	1362	US-10-054-534B-13	Sequence 13, Appl
3	1362	100.0	1362	US-10-431-952-13	Sequence 13, Appl
4	1362	100.0	1362	US-10-776-311-35	Sequence 35, Appl
5	641.6	47.1	1380	US-09-967-477B-7	Sequence 7, Appl
6	342.8	25.2	1434	US-10-250-821-3	Sequence 3, Appl
7	342.8	25.2	1434	US-10-250-553-3	Sequence 3, Appl
8	273.6	20.1	1374	US-10-840-478-25	Sequence 25, Appl
9	260.6	19.1	8894	US-10-840-325-124	Sequence 124, Appl
10	259.6	19.1	1374	US-10-278-391-3	Sequence 3, Appl
11	259.6	19.1	1374	US-10-840-478-1	Sequence 1, Appl

12	259.6	19.1	1374	US-10-840-325-36	Sequence 36, Appl
13	259.6	19.1	1617	US-10-776-311-33	Sequence 33, Appl
14	258	18.9	10328	US-10-840-325-129	Sequence 129, Appl
15	149.6	11.0	648	US-10-250-821-18	Sequence 18, Appl
16	149.6	11.0	648	US-10-250-553-18	Sequence 18, Appl
17	149.6	8.3	1095	US-10-156-761-2285	Sequence 2285, Appl
18	113.4	8.3	9025608	US-10-156-761-1	Sequence 1, Appl
19	107.2	7.9	2054	US-10-389-566-288	Sequence 288, Appl
20	106	7.8	1944	US-10-437-963-83761	Sequence 83761, A
21	91.4	6.7	1335	US-10-239-652A-4	Sequence 4, Appl
22	91.4	6.7	1474	US-09-925-298-232	Sequence 232, Appl
23	91.4	6.7	1474	US-10-102-806-232	Sequence 232, Appl
24	91.4	6.7	1575	US-10-264-237-670	Sequence 670, Appl
25	91.4	6.7	1686	US-10-191-513A-6	Sequence 6, Appl
26	91.4	6.7	1843	US-10-191-513A-7	Sequence 7, Appl
27	91.4	6.7	2257	US-10-191-513A-8	Sequence 8, Appl
28	91.4	6.7	2540	US-10-641-643-295	Sequence 295, Appl
29	91.4	6.7	3016	US-10-429-160-25	Sequence 25, Appl
30	91.4	6.7	3149	US-10-172-118-1010	Sequence 1010, Appl
31	91.4	6.7	3149	US-10-342-887-1010	Sequence 1010, Appl
32	91.4	6.7	3149	US-10-828-465-64	Sequence 64, Appl
33	89.6	6.6	883	US-09-823-245A-303	Sequence 303, Appl
34	89.6	6.6	1059	US-10-278-698-174	Sequence 174, Appl
35	89.6	6.6	1059	US-10-278-698-174	Sequence 174, Appl
36	89.6	6.6	1092	US-10-264-237-563	Sequence 563, Appl
37	89.6	6.6	1717	US-10-262-617-2	Sequence 2, Appl
38	89.6	6.6	1757	US-10-788-792-42	Sequence 42, Appl
39	89.6	6.6	1772	US-10-296-115-562	Sequence 562, Appl
40	89.4	6.6	1408	US-10-425-114-17460	Sequence 17460, A
41	89.2	6.5	1059	US-10-156-761-1580	Sequence 1580, Appl
42	87.4	6.4	347	US-09-796-692-4558	Sequence 4558, Appl
43	87.4	6.4	347	US-10-040-862-4558	Sequence 4558, Appl
44	87.4	6.4	347	US-10-057-475B-4558	Sequence 4558, Appl
45	87.4	6.4	347	US-10-154-884B-4558	Sequence 4558, Appl

#### ALIGNMENTS

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US-09-769-863-13  
Sequence 13, Application US/09769863  
Publication No. US20030157144A1  
GENERAL INFORMATION:  
APPLICANT: Abbott Laboratories  
APPLICANT: Mukerji, Pradip  
APPLICANT: Huang, Yung-Sheng  
APPLICANT: Dae, Tapas  
APPLICANT: Thurnmond, Jennifer  
APPLICANT: Pereira, Suzette L.  
TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF  
FILE REFERENCE: 6763.US.01  
CURRENT APPLICATION NUMBER: US/09/769, 863  
CURRENT FILING DATE: 2001-01-25  
NUMBER OF SEQ ID NOS: 32  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 1362  
TYPE: DNA  
ORGANISM: Saprolegnia diclina  
US-09-769-863-13

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Best Local Similarity 100.0%; Pred. No. 0;  
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61 CAAGACCAACCGGTGATCTGATCCACCAAGGTGTACCAATCTCGGCTTTGAGGAC 120

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: May 27, 2005, 00:54:26 ; Search time 264 Seconds  
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Gapop 10.0 , Gapept 1.0

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Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	259.6	19.1	1617	3	US-09-363-574-1
5	259.6	19.1	1617	3	US-09-363-526-1
6	259.6	19.1	1617	3	US-09-330-235-17
7	100.6	7.4	1281	4	US-09-857-583B-3
8	91.4	6.7	1686	3	US-09-439-261-6
9	91.4	6.7	1843	3	US-09-227-613-7
10	91.4	6.7	1843	3	US-09-439-261-7
11	91.4	6.7	1843	3	US-09-227-613-7
12	91.4	6.7	2257	3	US-09-439-261-8
13	91.4	6.7	2257	3	US-09-227-613-8
14	91.4	6.7	2540	4	US-09-023-655-295
15	91.4	6.7	3158	4	US-09-949-016-4613
16	89.6	6.6	1717	4	US-09-048-888-2
17	89.6	6.6	1758	4	US-09-948-016-4904
18	85.8	6.3	347	4	US-09-702-705-355
19	85.8	6.3	347	4	US-09-736-457-355
20	85.8	6.3	347	4	US-09-614-124B-355
21	85.8	6.3	347	4	US-09-671-325-355
22	85.8	6.3	347	4	US-09-589-184-355
23	85.8	6.3	347	4	US-09-658-824-355
24	77.6	5.7	1478	4	US-09-148-545-63
25	77.6	5.7	2016	4	US-09-148-545-119
26	70.2	5.2	1320	4	US-09-769-863-28
27	66	4.8	1702	3	US-08-934-254-26

28	66	4.8	1702	4	US-09-685-775-26	Sequence 26, Appl
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32	60	4.4	473	3	US-09-227-613-36	Sequence 36, Appl
33	60	4.4	655	3	US-09-439-261-3	Sequence 3, Appl
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42	56.6	4.2	10322	4	US-09-902-540-989	Sequence 5, Appl
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45	56.4	4.1	2277	2	US-09-098-487-5	Sequence 5, Appl

#### ALIGNMENTS

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US-09-769-863-13
; Sequence 13, Application US/09769863
; Patent No. 6635451
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Mukerji, Pradip
; APPLICANT: Huang, Yung-Sheng
; APPLICANT: Das, Tapas
; APPLICANT: Thurmond, Jennifer
; APPLICANT: Pereira, Suzette L.
; TITLE OF INVENTION: DESATURASE GENES AND USES THEREOF
; FILE REFERENCE: 6763 US. 01
; CURRENT APPLICATION NUMBER: US/09/769, 863
; CURRENT FILING DATE: 2001-01-25
; NUMBER OF SEQ. ID NOS: 32
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO: 13
; LENGTH: 1362
; TYPE: DNA
; ORGANISM: Saprolegnia diclina
US-09-769-863-13

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1362; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      61 CAAGACAACGCGGATCGATGATCCACACAGGTGTACGACATCTCGGGCTTTGAGGAC 120

QY      121 CACCCGGCGCGCTGTCATGTTTCAACGAGCGCGGCAAGACGCGACCGATGCTTGGCT 180
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QY      181 GTCTTCAACCGAGCTCGCGCTTCAAGCTCTCTGAGGATGTAAGTGTGCGAGCTGAC 240
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DB      241 CAGTCGACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 300

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ALIGNMENTS

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XX	OS	Saprolegnia diclina.							
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XX	PF	24-JAN-2002; 2002MO-US001924.							
XX	PR	25-JAN-2001; 2001US-00769863.							
XX	PR	22-JAN-2002; 2002US-00054534.							
XX	PA	(ABBO ) ABBOTT LAB.							
XX	PI	Mukerji P, Huang Y, Das T, Thurmond J, Pereira SL;							
XX	DR	WPI; 2003-067519/06.							
XX	DR	P-PDB; AAA89064.							
XX	PT	New delta 5 desaturase or delta 6 desaturase polypeptides, useful for producing polyunsaturated fatty acids, desaturates polyunsaturated fatty							

GenCore version 5.1.6  
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Post-processing: Minimum Match 0%  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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7	342.8	25.2	1434	6	AX951573 Sequence
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9	342.8	25.2	1669	6	AY082393 Phaeodact
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15	259.6	19.1	1617	6	AR098439 Sequence
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27	245.6	18.0	1374	8	AF306634 Mortierel
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ACCESSION AR410195  
VERSION AR410195.1 GI:40161436  
KEYWORDS  
SOURCE unknown.  
ORGANISM unknown.  
REFERENCE 1 (bases 1 to 1362)  
AUTHORS Mukerji, P., Huang, Y.-S., Das, T., Thurmond, J. and Pereira, S.L.  
TITLE Deaturase genes and uses thereof  
JOURNAL Patent: US 6635451-A 13 21-OCT-2003;  
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DB	1	ATGTCGAGGGGCAAAAGCCGGAAGATCTCGTGGCGGACCACTCCGAGCAACCGC	60		
QY	61	CAAGCAACGGGTGATCGTATCCACCAAGGTGTACGACATCTCGGCTTTAGGAC	120		
DB	61	CAAGCAACGGGTGATCGTATCCACCAAGGTGTACGACATCTCGGCTTTAGGAC	120		
QY	121	CACCGGGCGGCGTGTGATGATTCACGAGCGCGGCAAGACGCGATGCGTTCCT	180		
DB	121	CACCGGGCGGCGTGTGATGATTCACGAGCGCGGCAAGACGCGATGCGTTCCT	180		
QY	181	GTTTCACCGGAGTCTGAGCTCAAGCTCTCTGAGCGTACTAGTGGGAGCGTGCAC	240		
DB	181	GTTTCACCGGAGTCTGAGCTCAAGCTCTCTGAGCGTACTAGTGGGAGCGTGCAC	240		
QY	241	CAGTCGAGGGGCGGCGTGCACGCTGATCTCGGACGAGTCAAGAGGCAAGCGGAC	300		